Resource Summary Report

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ExPANdS

RRID:SCR_005199
Type: Tool

Proper Citation

ExPANdS (RRID:SCR_005199)

Resource Information

URL: http://cran.r-project.org/web/packages/expands/

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Description: Software that characterizes coexisting subpopulations (SPs) in a tumor using copy number and allele frequencies derived from exome- or whole genome sequencing input data. The model amplifies the statistical power to detect coexisting genotypes, by fully exploiting run-specific tradeoffs between depth of coverage and breadth of coverage. ExPANdS predicts the number of clonal expansions, the size of the resulting SPs in the tumor bulk, the mutations specific to each SP and tumor purity. The main function runExPANdS provides the complete functionality needed to predict coexisting SPs from single nucleotide variations (SNVs) and associated copy numbers. The robustness of the subpopulation predictions by ExPANdS increases with the number of mutations provided. It is recommended that at least 200 mutations are used as an input to obtain stable results.

Abbreviations: ExPANdS

Synonyms: Expanding Ploidy and Allele Frequency on Nested Subpopulations

Resource Type: software resource

Defining Citation: PMID:24177718

Keywords: copy number, allele, frequency, exome, whole genome, sequencing, ploidy, subpopulation, genotype, mutation, single nucleotide variation

Related Condition: Tumor

Availability: GNU General Public License, v2

Resource Name: ExPANdS

Resource ID: SCR_005199

Alternate IDs: OMICS_00218

Record Creation Time: 20220129T080228+0000

Record Last Update: 20260815T182301+0000

Ratings and Alerts

No rating or validation information has been found for ExPANdS.

No alerts have been found for ExPANdS.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 907 mentions in open access literature.

Listed below are recent publications. The full list is available at nidm-terms .

Schmidt H, et al. (2024) A regression based approach to phylogenetic reconstruction from multi-sample bulk DNA sequencing of tumors. PLoS computational biology, 20(12), e1012631.

Pithan L, et al. (2023) Closing the loop: autonomous experiments enabled by machine-learning-based online data analysis in synchrotron beamline environments. Journal of synchrotron radiation, 30(Pt 6), 1064.

Zhang W, et al. (2021) The bone microenvironment invigorates metastatic seeds for further dissemination. Cell, 184(9), 2471.

Bado IL, et al. (2021) The bone microenvironment increases phenotypic plasticity of ER+ breast cancer cells. Developmental cell, 56(8), 1100.

Yun JW, et al. (2019) Biomarkers Associated with Tumor Heterogeneity in Prostate Cancer. Translational oncology, 12(1), 43.

Oh BY, et al. (2019) Intratumor heterogeneity inferred from targeted deep sequencing as a prognostic indicator. Scientific reports, 9(1), 4542.

Little P, et al. (2019) Associating somatic mutations to clinical outcomes: a pan-cancer study of survival time. Genome medicine, 11(1), 37.

Morrissy AS, et al. (2017) Spatial heterogeneity in medulloblastoma. Nature genetics, 49(5), 780.

Sveen A, et al. (2017) Multilevel genomics of colorectal cancers with microsatellite instability-clinical impact of JAK1 mutations and consensus molecular subtype 1. Genome

medicine, 9(1), 46.

Zuo F, et al. (2014) Exploring population pharmacokinetic modeling with resampling visualization. BioMed research international, 2014, 585687.

Italiani P, et al. (2014) Transcriptomic profiling of the development of the inflammatory response in human monocytes in vitro. PloS one, 9(2), e87680.

Okada Y, et al. (2014) Integration of sequence data from a Consanguineous family with genetic data from an outbred population identifies PLB1 as a candidate rheumatoid arthritis risk gene. PloS one, 9(2), e87645.

Gibbons SM, et al. (2014) Human and environmental impacts on river sediment microbial communities. PloS one, 9(5), e97435.

Vaumourin E, et al. (2014) To be or not to be associated: power study of four statistical modeling approaches to identify parasite associations in cross-sectional studies. Frontiers in cellular and infection microbiology, 4, 62.

Nielsen NH, et al. (2014) Genetic diversity and population structure analysis of European hexaploid bread wheat (Triticum aestivum L.) varieties. PloS one, 9(4), e94000.

Hammerling D, et al. (2014) Completing the results of the 2013 Boston marathon. PloS one, 9(4), e93800.

Wurzbacher C, et al. (2014) Importance of saprotrophic freshwater fungi for pollen degradation. PloS one, 9(4), e94643.

Plomion C, et al. (2014) Genome-wide distribution of genetic diversity and linkage disequilibrium in a mass-selected population of maritime pine. BMC genomics, 15, 171.

Rylander C, et al. (2014) Consumption of lean fish reduces the risk of type 2 diabetes mellitus: a prospective population based cohort study of Norwegian women. PloS one, 9(2), e89845.

Dugas M, et al. (2014) Integrated data management for clinical studies: automatic transformation of data models with semantic annotations for principal investigators, data managers and statisticians. PloS one, 9(2), e90492.